

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/716,028

DATE: 02/14/2001
 TIME: 11:31:27

Input Set : A:\716028.txt
 Output Set: N:\CRF3\02142001\I716028.raw

3 <110> APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 5 <120> TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 7 <130> FILE REFERENCE: P1123R1
 9 <140> CURRENT APPLICATION NUMBER: US/09/716,028
 10 <141> CURRENT FILING DATE: 2000-11-17
 12 <150> PRIOR APPLICATION NUMBER: US 09/109,207
 13 <151> PRIOR FILING DATE: 1998-06-30
 14 <150> PRIOR APPLICATION NUMBER: US 60/051,554
 15 <151> PRIOR FILING DATE: 1997-07-03
 17 <160> NUMBER OF SEQ ID NOS: 44
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 6127
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial
 24 <220> FEATURE:
 W--> 25 <221> NAME/KEY: Artificial
 26 <222> LOCATION: 1-6127
 27 <223> OTHER INFORMATION: Expression plasmid
 29 <400> SEQUENCE: 1
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 34 gaactgtgtg cgcaggtaga agctttggag attatcgta ctgcaatgct 150
 36 tcgcaatatg gcgcaaaatg accaacagcg gttgattgat caggtagagg 200
 38 gggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250
 40 gagctgctgc gcgattacgt aaagaagtta ttgaagcatc ctcgtcagta 300
 42 aaaagttaat cttttcaaca gctgtcataa agttgtcagc gccgagactt 350
 44 atagtcgctt tgtttttatt ttttaagtta tttgttaacta gaattcgagc 400
 46 tcggtaccgc gggatcctct cgagggttgg gtgattttat gaaaaagaat 450
 48 atcgcatctt tccttgcatc tatgttcgtt ttttctattg ctacaaacgc 500
 50 gtacgctgat atccagctga cccagtcgcc gagctccctg tccgcctctg 550
 52 tgggcgtag ggtcaccatc acctgccgtg ccagtcagag cgtcgattac 600
 54 gaaggtgata gctacctgaa ctggtatcaa cagaaaccag gaaaagctcc 650
 56 gaaactactg atttacgcgg cctcgtacct ggagtctgga gtcccttctc 700
 58 gcttctctgg atccggttct gggacggatt tcactctgac catcagcagt 750
 60 ctgcagccag aagacttcgc aacttattac tgtcagcaaa gtcacgagga 800
 62 tccgtacaca tttggacagg gtaccaagggt ggagatcaaa cgaactgtgg 850
 64 ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct 900
 66 ggaactgctt ctgttgtgtg cctgctgaat aacttctatc ccagagaggc 950
 68 caaagtacag tggaaggtgg ataacgcctt ccaatcgggt aactcccagg 1000
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 74 cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag agcttcaaca 1150
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 78 acgcaagttc acgtaaaaag ggtatctaga ggttgagggtg attttatgaa 1250
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 82 caaacgcgta cgctgagggt cagctgggtg agtctggcgg tggcctgggtg 1350
 84 cagccagggg gctcactccg tttgtctgtg gcagtttctg gctactccat 1400

ENTERED

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90  agcgtcaagg  gccgtatcac  tataagtcgc  gacgattcca  aaaacacatt  1550
92  ctacctgcag  atgaacagcc  tgcgtgctga  ggacactgcc  gtctattatt  1600
94  gtgctcgagg  cagccactat  ttcgggtcact  ggcacttcgc  cgtgtggggg  1650
96  caaggaaccc  tggtcaccgt  ctccctcgcc  tccaccaagg  gcccatcggt  1700
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102 aactcaggcg  cctgaccag  cgcggtgcac  accttccccg  ctgtcctaca  1850
104 gtccctcagg  ctctactccc  tcagcagcgt  ggtgaccgtg  cctccagca  1900
106 gcttggggac  ccagacctac  atctgcaacg  tgaatcaca  gccagcaac  1950
108 accaaggtgg  acaagaaagt  tgagcccaaa  tcttgtgaca  aaactcacac  2000
110 ctagagtggc  ggtggctctg  gttccggtga  ttttgattat  gaaaagatgg  2050
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120 gacggtgata  attcaccttt  aatgaataat  ttccgtcaat  atttaccttc  2300
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140 tgccgatgat  cgtgtcctg  tcgttgagga  cccggttagg  ctggcggggg  2800
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156 ctctcgtttc  atcggtatca  ttaccccat  gaacagaaat  tcccccttac  3200
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164 tgagctttac  cgcaggatcc  ggaaattgta  aacgttaata  ttttgttaaa  3400
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168 aaatcggcaa  aatcccttat  aaatcaaaa  aatagaccga  gatagggttg  3500
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178 ggcgaacgtg  gcgagaaagg  aagggaagaa  agcgaaagga  gcgggcgcta  3750
180 gggcgctggc  aagtgtagcg  gtcacgctgc  gcgtaaccac  cacaccgcc  3800
182 gcgcttaatg  cgcgcgtaca  gggcgctgcc  ggatcctgcc  tcgcgcgttt  3850

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184  cggatgatgac ggtgaaaaacc tctgacacat gcagctcccg gagacgggtca 3900
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188  tcagcgggtg  ttggcgggtg tcggggcgca gccatgaccc agtcacgtag 4000
190  cgatagcgga  gtgtatactg gcttaactat gcggcatcag agcagattgt 4050
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198  aatacgggta  tccacagaat caggggataa cgcaggaaa aacatgtgag 4250
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234  ctgtctattt  cgttcaccca tagttgcctg actccccgtc gtgtagataa 5150
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262  cgtgcacca  actgatcttc agcatctttt actttcacca gcgtttctgg 5850
264  gtgagcaaaa  acagggaagg aaaaagcgc aaaaaagga ataaggcgca 5900
266  caccgaaatg  ttgaatactc atactcttcc tttttcaata ttattgaagc 5950
268  atttatcagg  gttattgtct catgagcgga tacatatattg aatgtattta 6000
270  gaaaaataaa  caaatagggg ttccgcgcac atttccccga aaagtgccac 6050
272  ctgacgtcta  agaaaccatt attatcatga cattaacctt taaaaatagg 6100
274  cgtatcacga  ggccctttcg tcttcaa 6127
276 <210> SEQ ID NO: 2
277 <211> LENGTH: 121
278 <212> TYPE: PRT

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279 <213> ORGANISM: Mus musculus
281 <400> SEQUENCE: 2
282 Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
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286           20           25           30
288 Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
289           35           40           45
291 Leu Glu Trp Met Gly Ser Ile Thr Tyr Asp Gly Ser Ser Asn Tyr
292           50           55           60
294 Asn Pro Ser Leu Lys Asn Arg Ile Ser Val Thr Arg Asp Thr Ser
295           65           70           75
297 Gln Asn Gln Phe Phe Leu Lys Leu Asn Ser Ala Thr Ala Glu Asp
298           80           85           90
300 Thr Ala Thr Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
301           95          100          105
303 Trp His Phe Ala Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
304          110          115          120
306 Ser
309 <210> SEQ ID NO: 3
310 <211> LENGTH: 121
311 <212> TYPE: PRT
312 <213> ORGANISM: Artificial
314 <220> FEATURE:
W--> 315 <221> NAME/KEY: Artificial
316 <222> LOCATION: 1-121
317 <223> OTHER INFORMATION: F(ab) sequence derived from MAE11
319 <400> SEQUENCE: 3
320 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
321   1           5           10           15
323 Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr
324           20           25           30
326 Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
327           35           40           45
329 Leu Glu Trp Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr
330           50           55           60
332 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
333           65           70           75
335 Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
336           80           85           90
338 Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
339           95          100          105
341 Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
342          110          115          120
344 Ser
347 <210> SEQ ID NO: 4
348 <211> LENGTH: 121
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens

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352 <220> FEATURE:
353 <221> NAME/KEY: unsure
354 <222> LOCATION: 30, 104-108
355 <223> OTHER INFORMATION: unknown amino acid
357 <400> SEQUENCE: 4
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359 1 5 10 15
W--> 361 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa
362 20 25 30
364 Ser Asp Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
365 35 40 45
367 Leu Glu Trp Val Ala Val Ile Ser Asn Gly Ser Asp Thr Tyr Tyr
368 50 55 60
370 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
371 65 70 75
373 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
374 80 85 90
W--> 376 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Arg Phe Phe Xaa Xaa
377 95 100 105
W--> 379 Xaa Xaa Xaa Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
380 110 115 120
382 Ser
385 <210> SEQ ID NO: 5
386 <211> LENGTH: 111
387 <212> TYPE: PRT
388 <213> ORGANISM: Mus musculus
390 <400> SEQUENCE: 5
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392 1 5 10 15
394 Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp
395 20 25 30
397 Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
398 35 40 45
400 Gln Pro Pro Ile Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Gly Ser
401 50 55 60
403 Glu Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
404 65 70 75
406 Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Phe
407 80 85 90
409 Tyr Cys Gln Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Ala Gly
410 95 100 105
412 Thr Lys Leu Glu Ile Lys
413 110
415 <210> SEQ ID NO: 6
416 <211> LENGTH: 111
417 <212> TYPE: PRT
418 <213> ORGANISM: Artificial
420 <220> FEATURE:
W--> 421 <221> NAME/KEY: Artificial

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L:25 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:315 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:421 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:491 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:526 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:561 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:596 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:631 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:666 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
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L:1444 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:1500 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:1559 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
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L:1711 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:1726 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:1739 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:1749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1757 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1775 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:1803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1811 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:1821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1831 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:1841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1849 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42

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L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1869 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1889 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
L:1899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44